BOLD

(Ribosome Binding Site) (Start Codon)

CGGGAGCTTG**AAGGA**CACAAGAATGGGAGGAAAGGCGGACTCTCAGGAAC TTCATTCTTCACGTGGTTT**ATG**GTGATTGCATTGCTGGGCGTCTGGACAT CTGTAGCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGGA AAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGA TGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAG TCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCT GTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCA GTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACT TGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAG TTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGA AGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTT CACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAAT CCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATAC AGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTC TAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGAT AATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCC TGTGGAAGAACAGCAGGAAGTACCACCAGATACT**TAA**AGCTTCAAAAAGA CTGCCCCTACCACACAGGAGGACCAGCCTAACCATACGCTCCAAAAGAT GGCTGTGATAGATCTTGTGAAGCAATTACTGAGCAGATCAAGATCTTTGG GAAGGAACACTAAAGATGTTTTGAATGAATTATAGTCCACTGGCATTTTA GTGTATTTTTTTTTTTTTAGAAACACACATTTCTAAAAATGTCATGTT ACATTCCTGCATGTCCCTTTTGATAGCATTAGTGGATCCATTGGATTTCT TTTTTCTTTTGTGAGACAGCTTTTAGTCTTACCTGA**ATTTA**TGTGTGTT TTTCCGACAGTGGTTAATAATTATATTGGTGATGTAGCAGCAATTGTGTT GGCAGGGTTTTCATATATTATTAGTAATTAACACTAACTGTTGGACTGAC TTGTGTACACTGTGTTAAACATG**ATTTA**AAAGCTATTAAGAGTACTTTGT GTTAGCACTCTTAAAAACGCTAACAGAGATCATCATTAGCTGTGAAGATT TGAGTTGTATATACCTGCACTGATATTCTTATCAAAAATTTCTACATTAG CTTTAAGTGTTCAGATTAACACTTTTGAAACCTTTGTAGCTTTTAGCTGA TTAATTAGAAAATTAATATTTCAGTGAAAGTTTTAAATTATC**ATTTA**TT TATTTTTTAAATGAGAGGGGAAAGCTGAAATTCCTTGTTAAGACACAAG GAAAAAGAATGGCCCTACTATTATCATGCAAAAATGCTTTGTTGGCACCT CAGATTAATCATATAATAGCTATAGTCTCTTCAGCATTTGTTTAAATTTT AGAAAACCTGTATAAATTACTGGTGCATAACTTAAAGATTATTCTGCCTT TGGCTAATTGAGTAATTCCCCTCCAGCACTAGAGACCGCTCAGTGCTCTT AAAAGCTCACAGAGCCCGATGCCTGCTGCTATTTCACGGCAATGAGCCTT TTTCTTTCTACACTGAAGATTTTCTTCTT**ATTTA**ATGTGGTTTATTTTGG GCTCAGAAATAATTGCTCTGTTGAAAATAATCCTTTGTCAGAAAAGAAGG TAGCTACCACATCATTTGAAAGGACCATGAGCAACTATAAGCAAAGCCA TAAGAAGTGGTTTGATCGATATATTAGGGGGTAGCTCTTGATTTTGTTAAC ATTAAGATAAGGTGACTTTTTCCCCCTGCTTTTAGG**ATTAAAA**TCAAAGA TACTTCTATATTTTTATCACTATAGATCATAGTTATTATACAATGTAGTG AGTCCTGCATGGGTACTCGATGTAATGAAACCTGAAATAATAATAAGA TAATAAGAAAAGCAATAATTTTCTAAAGCTGTGCTGTCGGTGATACAGAG ATGATACTCAAATTAT**AATAAA**ACTCTTCATTTTGTGAATTATAGAAGCT ACTTTTTATAAAGCCATATTTTTTTAGGGAAACTAAGGAGTGACATAGAA CTGATGAATGAGTAAAAGTAAGTTTTGCTGGATTTTTGTAGAACTCTGGA

CGTTGAGGATTCATTATGCTGTGGTTAACTTTTAAATATTTTT

{Stop Codon}

(Instability Sequence

{Instability Sequence}

{Instability Sequence}

(Instability Sequence)

{Sub-optimal Polyadenylation Site}

(Optimal Polyadenylation Site

ladcfrufdknadgfidieelgeilrat

COMPUTER PREDICTED DOMAINS IN LABYRINTHIN

EIA TURE AMYD	SAW AA MICHTAN DIEGEATA	(LGI I DADG DGDI D V DDAK V HLGHK
-		^
ERSTSEPAVPF	\ PEEAEPHTEPEEQVPVE!	AEPQNIEDEAKEQIQSLLHEMVHAE ',
	,	
HVEGEDLQQED)GPTGEPQQEDDEFLMA	TOVDDRFETLEPEVSHEETEHSYHV \
EETVSQDCNQD	DMEEMMSEQENPDSSEP	VVEDERLHHDTDDvtyqvyeeqavY \ \ <mad i=""> \</mad>
EDI ENECTETO		iveevsifpvEEQQEVPPDT
EALTENE GIETI		MAD/II-> '
		\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
•		VLGKLGIYDADGDGDFDVDDAKVLLGLK
	Parvalbumin	vkkafaildqdksqfieedelklflqnf &kaafslfdkaddatittkelatvmrsl

SYMBOL KEY

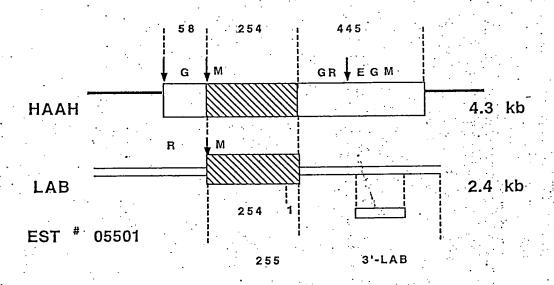
BOLD = Eukaryotic Leader Sequence

= Myristylation site

lower case = Membrane Anchoring Domian (MAD)

Troponin-C

Ca⁺⁺ Binding Residues Required residue



 ↓ = Start Colon
 R = Ribosome Binding Site
 E = Enzymatic Site
 G = Glycosylation Site
 M = Membrane Anchoring Domain
 3'-LAB = Contains poly A signal (x2); instabilty sequence (x4)